

# SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: ARIYASU, Toshio  
NAKAMURA, Shuji  
ORITA, Kunzo
- (ii) TITLE OF INVENTION: HEDGEHOG PROTEIN
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: BROWDY AND NEIMARK
  - (B) STREET: 419 Seventh Street N.W., Ste. 300
  - (C) CITY: Washington
  - (D) STATE: D.C.
  - (E) COUNTRY: United States of America
  - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/063,778
  - (B) FILING DATE: 22-APR-1998
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: JP 97-121578
  - (B) FILING DATE: 25-APR-1997
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: JP 98-
  - (B) FILING DATE: 14-APR-1998
- (ix) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Browdy, Roger L.
  - (B) REGISTRATION NUMBER: 25,618
  - (C) REFERENCE/DOCKET NUMBER: ARIYASU=1
- (x) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (202) 628-5197
  - (B) TELEFAX: (202) 737-35281

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 176 amino acids  
 (B) TYPE: amino acid  
 (C) strandedness: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Cys Gly Pro Gly Arg Gly Pro Val Gly Arg Arg Arg Tyr Ala Arg Lys  
1 5 10 15

Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe Val Pro Gly Val Pro Glu  
                   20                                  25                                  30  
 Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu Gly Arg Val Ala Arg Gly  
                   35                                  40                                  45  
 Ser Glu Arg Phe Arg Asp Leu Val Pro Asn Tyr Asn Pro Asp Ile Ile  
                   50                                  55                                  60  
 Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp Arg Leu Met Thr Glu Arg  
                   65                                  70                                  75                                  80  
 Cys Lys Glu Arg Val Asn Ala Leu Ala Ile Ala Val Met Asn Met Trp  
                                   85                                  90                                  95  
 Pro Gly Val Arg Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His  
                                   100                                  105                                  110  
 His Ala Gln Asp Ser Leu His Tyr Glu Gly Arg Ala Leu Asp Ile Thr  
                   115                                  120                                  125  
 Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala  
                   130                                  135                                  140  
 Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Arg Asn His Ile  
                   145                                  150                                  155                                  160  
 His Val Ser Val Lys Ala Asp Asn Ser Leu Ala Val Arg Ala Gly Gly  
                                   165                                  170                                  175

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1..176
- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Cys Gly Pro Gly Arg Gly Pro Val Gly Arg Arg Arg Tyr Ala Arg Lys  
   1                                  5                                  10                                  15  
 Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe Val Pro Gly Val Pro Glu  
                   20                                  25                                  30  
 Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu Gly Arg Val Ala Arg Gly  
                   35                                  40                                  45  
 Ser Glu Arg Phe Arg Asp Leu Val Pro Asn Tyr Asn Pro Asp Ile Ile  
                   50                                  55                                  60  
 Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp Arg Leu Met Thr Glu Arg  
                   65                                  70                                  75                                  80

Cys Lys Glu Arg Val Asn Ala Leu Ala Ile Ala Val Met Asn Met Trp  
                                     85                                    90                                    95  
 Pro Gly Val Arg Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His  
                                     100                                    105                                    110  
 His Ala Gln Asp Ser Leu His Tyr Glu Gly Arg Ala Leu Asp Ile Thr  
                                     115                                    120                                    125  
 Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala  
                                     130                                    135                                    140  
 Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Arg Asn His Ile  
                                     145                                    150                                    155                                    160  
 His Val Ser Val Lys Ala Asp Asn Ser Leu Ala Val Arg Ala Gly Gly  
                                     165                                    170                                    175  
 Cys Phe Pro Gly Asn Ala Thr Val Arg Leu Trp Ser Gly Glu Arg Lys  
                                     180                                    185                                    190  
 Gly Leu Arg Glu Leu His Arg Gly Asp Trp Val Leu Thr Ala Asp Ala  
                                     195                                    200                                    205  
 Ser Gly Arg Val Val Pro Thr Pro Val Leu Leu Phe Leu Asp Arg Asp  
                                     210                                    215                                    220  
 Leu Gln Arg Arg Ala Ser Phe Val Ala Val Glu Thr Glu Trp Pro Pro  
                                     225                                    230                                    235                                    240  
 Arg Lys Leu Leu Leu Thr Pro Trp His Leu Val Phe Ala Ala Arg Gly  
                                     245                                    250                                    255  
 Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro Val Phe Ala Arg Arg Leu  
                                     260                                    265                                    270  
 Arg Ala Gly Asp Ser Val Leu Ala Pro Gly Gly Asp Ala Leu Arg Pro  
                                     275                                    280                                    285  
 Ala Arg Val Ala Arg Val Ala Arg Glu Glu Ala Val Gly Val Phe Ala  
                                     290                                    295                                    300  
 Pro Leu Thr Ala His Gly Thr Leu Leu Val Asn Asp Val Leu Ala Ser  
                                     305                                    310                                    315                                    320  
 Cys Tyr Ala Val Leu Glu Ser His Gln Trp Ala His Arg Ala Phe Ala  
                                     325                                    330                                    335  
 Pro Leu Arg Leu Leu His Ala Leu Gly Ala Leu Leu Pro Gly Gly Ala  
                                     340                                    345                                    350  
 Val Gln Pro Thr Gly Met His Trp Tyr Ser Arg Leu Leu Tyr Arg Leu  
                                     355                                    360                                    365  
 Ala Glu Glu Leu Leu Gly  
                                     370

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 amino acids  
 (B) TYPE: amino acid  
 (C) strandedness: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: sig peptide  
 (B) LOCATION: -22..-1  
 (C) IDENTIFICATION METHOD: S  
 (A) NAME/KEY: mat peptide  
 (B) LOCATION: 1..176  
 (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
  -20                      -15                      -10

Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
  -5                      1                      5                      10

Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
          15                      20                      25

Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
          30                      35                      40

Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
  45                      50                      55

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
  60                      65                      70

Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
  75                      80                      85                      90

Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
          95                      100                      105

Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
  110                      115                      120

Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
  125                      130                      135

Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
  140                      145                      150

Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
  155                      160                      165                      170

Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
          175                      180                      185

Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
  190                      195                      200

Val Leu Thr Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu
  205                      210                      215
  
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Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val  
 220 225 230  
 Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu  
 235 240 245 250  
 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro  
 255 260 265  
 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly  
 270 275 280  
 Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu  
 285 290 295  
 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val  
 300 305 310  
 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp  
 315 320 325 330  
 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala  
 335 340 345  
 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser  
 350 355 360  
 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly  
 365 370

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1..528
- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TGC	GGG	CCG	GGC	CGG	GGG	CCG	GTT	GGC	CGG	CGC	CGC	TAT	GCG	CGC	AAG	48
Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg	Arg	Arg	Tyr	Ala	Arg	Lys	
1				5				10						15		
CAG	CTC	GTG	CCG	CTA	CTC	TAC	AAG	CAA	TTT	GTG	CCC	GGC	GTG	CCA	GAG	96
Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe	Val	Pro	Gly	Val	Pro	Glu	
			20				25					30				
CGG	ACC	CTG	GGC	GCC	AGT	GGG	CCA	GCG	GAG	GGG	AGG	GTG	GCA	AGG	GGC	144
Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	Gly	Arg	Val	Ala	Arg	Gly	
			35				40					45				

TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC TAC AAC CCC GAC ATC ATC	192
Ser Glu Arg Phe Arg Asp Leu Val Pro Asn Tyr Asn Pro Asp Ile Ile	
50 55 60	
TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC CGC CTG ATG ACC GAA CGT	240
Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp Arg Leu Met Thr Glu Arg	
65 70 75 80	
TGT AAG GAA CGG GTG AAC GCT TTG GCC ATT GCC GTG ATG AAC ATG TGG	288
Cys Lys Glu Arg Val Asn Ala Leu Ala Ile Ala Val Met Asn Met Trp	
85 90 95	
CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC TGG GAC GAG GAC GGC CAC	336
Pro Gly Val Arg Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His	
100 105 110	
CAC GCT CAG GAT TCA CTC CAC TAC GAA GGC CGT GCT TTG GAC ATC ACT	384
His Ala Gln Asp Ser Leu His Tyr Glu Gly Arg Ala Leu Asp Ile Thr	
115 120 125	
ACG TCT GAC CGC GAC CGC AAC AAG TAT GGG TTG CTG GCG CGC CTC GCA	432
Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala	
130 135 140	
GTG GAA GCC GGC TTC GAC TGG GTC TAC TAC GAG TCC CGC AAC CAC ATC	480
Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Arg Asn His Ile	
145 150 155 160	
CAC GTG TCG GTC AAA GCT GAT AAC TCA CTG GCG GTC CGG GCG GGC GGC	528
His Val Ser Val Lys Ala Asp Asn Ser Leu Ala Val Arg Ala Gly Gly	
165 170 175	

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1..528
- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG CGC CGC TAT GCG CGC AAG	48
Cys Gly Pro Gly Arg Gly Pro Val Gly Arg Arg Arg Tyr Ala Arg Lys	
1 5 10 15	
CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT GTG CCC GGC GTG CCA GAG	96
Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe Val Pro Gly Val Pro Glu	
20 25 30	
CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG GGG AGG GTG GCA AGG GGC	144
Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu Gly Arg Val Ala Arg Gly	
35 40 45	

TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC TAC AAC CCC GAC ATC ATC	192
Ser Glu Arg Phe Arg Asp Leu Val Pro Asn Tyr Asn Pro Asp Ile Ile	
50 55 60	
TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC CGC CTG ATG ACC GAA CGT	240
Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp Arg Leu Met Thr Glu Arg	
65 70 75 80	
TGT AAG GAA CGG GTG AAC GCT TTG GCC ATT GCC GTG ATG AAC ATG TGG	288
Cys Lys Glu Arg Val Asn Ala Leu Ala Ile Ala Val Met Asn Met Trp	
85 90 95	
CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC TGG GAC GAG GAC GGC CAC	336
Pro Gly Val Arg Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His	
100 105 110	
CAC GCT CAG GAT TCA CTC CAC TAC GAA GGC CGT GCT TTG GAC ATC ACT	384
His Ala Gln Asp Ser Leu His Tyr Glu Gly Arg Ala Leu Asp Ile Thr	
115 120 125	
ACG TCT GAC CGC GAC CGC AAC AAG TAT GGG TTG CTG GCG CGC CTC GCA	432
Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala	
130 135 140	
GTG GAA GCC GGC TTC GAC TGG GTC TAC TAC GAG TCC CGC AAC CAC ATC	480
Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Arg Asn His Ile	
145 150 155 160	
CAC GTG TCG GTC AAA GCT GAT AAC TCA CTG GCG GTC CGG GCG GGC GGC	528
His Val Ser Val Lys Ala Asp Asn Ser Leu Ala Val Arg Ala Gly Gly	
165 170 175	
TGC TTT CCG GGA AAT GCA ACT GTG CGC CTG TGG AGC GGC GAG CGG AAA	576
Cys Phe Pro Gly Asn Ala Thr Val Arg Leu Trp Ser Gly Glu Arg Lys	
180 185 190	
GGG CTG CGG GAA CTG CAC CGC GGA GAC TGG GTT TTG ACG GCC GAT GCG	624
Gly Leu Arg Glu Leu His Arg Gly Asp Trp Val Leu Thr Ala Asp Ala	
195 200 205	
TCA GGC CGG GTG GTG CCC ACG CCG GTG CTG CTC TTC CTG GAC CGG GAC	672
Ser Gly Arg Val Val Pro Thr Pro Val Leu Leu Phe Leu Asp Arg Asp	
210 215 220	
TTG CAG CGC CGG GCT TCA TTT GTG GCT GTG GAG ACC GAG TGG CCT CCA	720
Leu Gln Arg Arg Ala Ser Phe Val Ala Val Glu Thr Glu Trp Pro Pro	
225 230 235 240	
CGC AAA CTG TTG CTC ACG CCC TGG CAC CTG GTG TTT GCC GCT CGA GGG	768
Arg Lys Leu Leu Leu Thr Pro Trp His Leu Val Phe Ala Ala Arg Gly	
245 250 255	
CCG GCG CCC GCG CCA GGC GAC TTT GCA CCG GTG TTC GCG CGC CGG CTA	816
Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro Val Phe Ala Arg Arg Leu	
260 265 270	
CGC GCT GGG GAC TCG GTG CTG GCG CCC GGC GGG GAT GCG CTT CGG CCA	864
Arg Ala Gly Asp Ser Val Leu Ala Pro Gly Gly Asp Ala Leu Arg Pro	
275 280 285	

GCG	CGC	GTG	GCC	CGT	GTG	GCG	CGG	GAG	GAA	GCC	GTG	GGC	GTG	TTC	GCG	912
Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu	Ala	Val	Gly	Val	Phe	Ala	
290						295					300					
CCG	CTC	ACC	GCG	CAC	GGG	ACG	CTG	CTG	GTG	AAC	GAT	GTC	CTG	GCC	TCT	960
Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val	Asn	Asp	Val	Leu	Ala	Ser	
305					310					315					320	
TGC	TAC	GCG	GTT	CTG	GAG	AGT	CAC	CAG	TGG	GCG	CAC	CGC	GCT	TTT	GCC	1008
Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp	Ala	His	Arg	Ala	Phe	Ala	
				325					330					335		
CCC	TTG	AGA	CTG	CTG	CAC	GCG	CTA	GGG	GCG	CTG	CTC	CCC	GGC	GGG	GCC	1056
Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala	Leu	Leu	Pro	Gly	Gly	Ala	
			340					345					350			
GTC	CAG	CCG	ACT	GGC	ATG	CAT	TGG	TAC	TCT	CGG	CTC	CTC	TAC	CGC	TTA	1104
Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser	Arg	Leu	Leu	Tyr	Arg	Leu	
		355					360					365				
GCG	GAG	GAG	CTA	CTG	GCG											1122
Ala	Glu	Glu	Leu	Leu	Gly											
370																

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: sig peptide
- (B) LOCATION: 1..66
- (C) IDENTIFICATION METHOD: S
- (A) NAME/KEY: mat peptide
- (B) LOCATION: 67..594
- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ATG	GCT	CTC	CTG	ACC	AAT	CTA	CTG	CCC	CTG	TGC	TGC	TTG	GCA	CTT	CTG	48
Met	Ala	Leu	Leu	Thr	Asn	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu	
	-20					-15						-10				
GCG	CTG	CCA	GCC	CAG	AGC	TGC	GGG	CCG	GGC	CGG	GGG	CCG	GTT	GGC	CGG	96
Ala	Leu	Pro	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg	
-5				1					5					10		
CGC	CGC	TAT	GCG	CGC	AAG	CAG	CTC	GTG	CCG	CTA	CTC	TAC	AAG	CAA	TTT	144
Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe	
			15					20					25			
GTG	CCC	GGC	GTG	CCA	GAG	CGG	ACC	CTG	GGC	GCC	AGT	GGG	CCA	GCG	GAG	192
Val	Pro	Gly	Val	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	
		30						35					40			



GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC	240
Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	
45 50 55	
TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC	288
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	
60 65 70	
CGC CTG ATG ACC GAA CGT TGT AAG GAA CGG GTG AAC GCT TTG GCC ATT	336
Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	
75 80 85 90	
GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC	384
Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
95 100 105	
TGG GAC GAG GAC GGC CAC CAC GCT CAG GAT TCA CTC CAC TAC GAA GGC	432
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
110 115 120	
CGT GCT TTG GAC ATC ACT ACG TCT GAC CGC GAC CGC AAC AAG TAT GGG	480
Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
125 130 135	
TTG CTG GCG CGC CTC GCA GTG GAA GCC GGC TTC GAC TGG GTC TAC TAC	528
Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
140 145 150	
GAG TCC CGC AAC CAC ATC CAC GTG TCG GTC AAA GCT GAT AAC TCA CTG	576
Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu	
155 160 165 170	
GCG GTC CGG GCG GGC GGC TGC TTT CCG GGA AAT GCA ACT GTG CGC CTG	624
Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu	
175 180 185	
TGG AGC GGC GAG CGG AAA GGG CTG CGG GAA CTG CAC CGC GGA GAC TGG	672
Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp	
190 195 200	
GTT TTG ACG GCC GAT GCG TCA GGC CGG GTG GTG CCC ACG CCG GTG CTG	720
Val Leu Thr Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu	
205 210 215	
CTC TTC CTG GAC CGG GAC TTG CAG CGC CGG GCT TCA TTT GTG GCT GTG	768
Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val	
220 225 230	
GAG ACC GAG TGG CCT CCA CGC AAA CTG TTG CTC ACG CCC TGG CAC CTG	816
Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu	
235 240 245 250	
GTG TTT GCC GCT CGA GGG CCG GCG CCC GCG CCA GGC GAC TTT GCA CCG	864
Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro	
255 260 265	
GTG TTC GCG CGC CGG CTA CGC GCT GGG GAC TCG GTG CTG GCG CCC GGC	912
Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly	
270 275 280	

GGG GAT GCG CTT CGG CCA GCG CGC GTG GCC CGT GTG GCG CGG GAG GAA 960  
 Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu  
 285 290 295

GCC GTG GGC GTG TTC GCG CCG CTC ACC GCG CAC GGG ACG CTG CTG GTG 1008  
 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val  
 300 305 310

AAC GAT GTC CTG GCC TCT TGC TAC GCG GTT CTG GAG AGT CAC CAG TGG 1056  
 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp  
 315 320 325 330

GCG CAC CGC GCT TTT GCC CCC TTG AGA CTG CTG CAC GCG CTA GGG GCG 1104  
 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala  
 335 340 345

CTG CTC CCC GGC GGG GCC GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT 1152  
 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser  
 350 355 360

CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CTG GGC 1188  
 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly  
 365 370

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (B) INDIVIDUAL ISOLATE: ARH-77, ATCC CRL-1621

(ix) FEATURE:

- (A) NAME/KEY: sig peptide
- (B) LOCATION: 1..18
- (C) IDENTIFICATION METHOD: S
- (A) NAME/KEY: mat peptide
- (B) LOCATION: 19..546
- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG 48  
 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg  
 -5 1 5 10

CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT 96  
 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe  
 15 20 25

GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG 144  
 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu  
 30 35 40

GGG	AGG	GTG	GCA	AGG	GGC	TCC	GAG	CGC	TTC	CGG	GAC	CTC	GTG	CCC	AAC	192
Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn	
		45					50					55				
TAC	AAC	CCC	GAC	ATC	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGT	GGA	GCC	GAC	240
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
	60					65					70					
CGC	CTG	ATG	ACC	GAA	CGT	TGT	AAG	GAA	CGG	GTG	AAC	GCT	TTG	GCC	ATT	288
Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
	75				80					85					90	
GCC	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTG	CGC	CTA	CGA	GTG	ACT	GAG	GGC	336
Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
				95				100						105		
TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCT	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	384
Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
			110					115					120			
CGT	GCT	TTG	GAC	ATC	ACT	ACG	TCT	GAC	CGC	GAC	CGC	AAC	AAG	TAT	GGG	432
Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
		125					130					135				
TTG	CTG	GCG	CGC	CTC	GCA	GTG	GAA	GCC	GGC	TTC	GAC	TGG	GTC	TAC	TAC	480
Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
	140					145					150					
GAG	TCC	CGC	AAC	CAC	ATC	CAC	GTG	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	528
Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
	155				160					165					170	
GCG	GTC	CGG	GCG	GGC	GGC	TG										548
Ala	Val	Arg	Ala	Gly	Gly											
				175												

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (B) INDIVIDUAL ISOLATE: ARH-77, ATCC CRL-1621

(ix) FEATURE:

- (A) NAME/KEY: 5pUTR
- (B) LOCATION: 1..6
- (C) IDENTIFICATION METHOD: S
- (A) NAME/KEY: sig peptide
- (B) LOCATION: 7..72
- (C) IDENTIFICATION METHOD: S
- (A) NAME/KEY: mat peptide
- (B) LOCATION: 73..600
- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GTATCC ATG GCT CTC CTG ACC AAT CTA CTG CCC CTG TGC TGC TTG GCA	48
Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala	
-20 -15 -10	
CTT CTG GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT	96
Leu Leu Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val	
-5 1 5	
GGC CGG CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG	144
Gly Arg Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys	
10 15 20	
CAA TTT GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA	192
Gln Phe Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro	
25 30 35 40	
GCG GAG GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG	240
Ala Glu Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val	
45 50 55	
CCC AAC TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA	288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly	
60 65 70	
GCC GAC CGC CTG ATG ACC GAA CGT TGT AAG GAA CGG GTG AAC GCT TTG	336
Ala Asp Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu	
75 80 85	
GCC ATT GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT	384
Ala Ile Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr	
90 95 100	
GAG GGC TGG GAC GAG GAC GGC CAC CAC GCT CAG GAT TCA CTC CAC TAC	432
Glu Gly Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr	
105 110 115 120	
GAA GGC CGT GCT TTG GAC ATC ACT ACG TCT GAC CGC GAC CGC AAC AAG	480
Glu Gly Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys	
125 130 135	
TAT GGG TTG CTG GCG CGC CTC GCA GTG GAA GCC GGC TTC GAC TGG GTC	528
Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
140 145 150	
TAC TAC GAG TCC CGC AAC CAC ATC CAC GTG TCG GTC AAA GCT GAT AAC	576
Tyr Tyr Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn	
155 160 165	
TCA CTG GCG GTC CGG GCG GGC GGC TG	602
Ser Leu Ala Val Arg Ala Gly Gly	
170 175	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(B) INDIVIDUAL ISOLATE: ARH-77, ATCC CRL-1621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
C GTG TCG GTC AAA GCT GAT AAC TCA CTG GCG GTC CGG GCG GGC GGC      46
  Val Ser Val Lys Ala Asp Asn Ser Leu Ala Val Arg Ala Gly Gly
    1             5             10             15

TGC TTT CCG GGA AAT GCA ACT GTG CGC CTG TGG AGC GGC GAG CGG AAA      94
  Cys Phe Pro Gly Asn Ala Thr Val Arg Leu Trp Ser Gly Glu Arg Lys
                20             25             30

GGG CTG CGG GAA CTG CAC CGC GGA GAC TGG GTT TTG ACG GCC GAT GCG      142
  Gly Leu Arg Glu Leu His Arg Gly Asp Trp Val Leu Thr Ala Asp Ala
                35             40             45

TCA GGC CGG GTG GTG CCC ACG CCG GTG CTG CTC TTC CTG GAC CGG GAC      190
  Ser Gly Arg Val Val Pro Thr Pro Val Leu Leu Phe Leu Asp Arg Asp
                50             55             60

TTG CAG CGC CGG GCT TCA TTT GTG GCT GTG GAG ACC GAG TGG CCT CCA      238
  Leu Gln Arg Arg Ala Ser Phe Val Ala Val Glu Thr Glu Trp Pro Pro
                65             70             75

CGC AAA CTG TTG CTC ACG CCC TGG CAC CTG GTG TTT GCC GCT CGA GGG      286
  Arg Lys Leu Leu Leu Thr Pro Trp His Leu Val Phe Ala Ala Arg Gly
                80             85             90             95

CCG GCG CCC GCG CCA GGC GAC TTT GCA CCG GTG TTC GCG CGC CGG CTA      334
  Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro Val Phe Ala Arg Arg Leu
                100            105            110

CGC GCT GGG GAC TCG GTG CTG GCG CCC GGC GGG GAT GCG CTT CGG CCA      382
  Arg Ala Gly Asp Ser Val Leu Ala Pro Gly Gly Asp Ala Leu Arg Pro
                115            120            125

GCG CGC GTG GCC CGT GTG GCG CGG GAG GAA GCC GTG GGC GTG TTC GCG      430
  Ala Arg Val Ala Arg Val Ala Arg Glu Glu Ala Val Gly Val Phe Ala
                130            135            140

CCG CTC ACC GCG CAC GGG ACG CTG CTG GTG AAC GAT GTC CTG GCC TCT      478
  Pro Leu Thr Ala His Gly Thr Leu Leu Val Asn Asp Val Leu Ala Ser
                145            150            155

TGC TAC GCG GTT CTG GAG AGT CAC CAG TGG GCG CAC CGC GCT TTT GCC      526
  Cys Tyr Ala Val Leu Glu Ser His Gln Trp Ala His Arg Ala Phe Ala
                160            165            170            175

CCC TTG AGA CTG CTG CAC GCG CTA GGG GCG CTG CTC CCC GGC GGG GCC      574
  Pro Leu Arg Leu Leu His Ala Leu Gly Ala Leu Leu Pro Gly Gly Ala
                180            185            190
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G

575

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (B) INDIVIDUAL ISOLATE: ARH-77, ATCC CRL-1621

(ix) FEATURE:

- (A) NAME/KEY: 3pUTR
- (B) LOCATION: 218..230
- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

G	TTC	GCG	CCG	CTC	ACC	GCG	CAC	GGG	ACG	CTG	CTG	GTG	AAC	GAT	GTC	46
	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val	Asn	Asp	Val	
1					5					10					15	
CTG	GCC	TCT	TGC	TAC	GCG	GTT	CTG	GAG	AGT	CAC	CAG	TGG	GCG	CAC	CGC	94
	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp	Ala	His	Arg
				20					25					30		
GCT	TTT	GCC	CCC	TTG	AGA	CTG	CTG	CAC	GCG	CTA	GGG	GCG	CTG	CTC	CCC	142
	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala	Leu	Leu	Pro
				35					40					45		
GGC	GGG	GCC	GTC	CAG	CCG	ACT	GGC	ATG	CAT	TGG	TAC	TCT	CGG	CTC	CTC	190
	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser	Arg	Leu	Leu
			50					55					60			
TAC	CGC	TTA	GCG	GAG	GAG	CTA	CTG	GGC	TGAGCGTCCC	AGG						230
	Tyr	Arg	Leu	Ala	Glu	Glu	Leu	Leu	Gly							
	65							70								

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (B) INDIVIDUAL ISOLATE: A549, ATCC CRL-185

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1..522
- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGC GGA CCG GGC AGG GGG TTC GGG AAA AGG AGG CAC CCC AAA AAG CTG	48
Cys Gly Pro Gly Arg Gly Phe Gly Lys Arg Arg His Pro Lys Lys Leu	
1 5 10 15	
ACC CCT TTA GCC TAC AAG CAG TTT ATC CCC AAT GTG GCC GAA AAG ACC	96
Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr	
20 25 30	
CTA GGC GCC AGC GGA AGG TAT GAA GGG AAG ATC TCC AGA AAC TCC GAG	144
Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Ser Arg Asn Ser Glu	
35 40 45	
CGA TTT AAG GAA CTC ACC CCC AAT TAC AAC CCC GAC ATC ATA TTT AAG	192
Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys	
50 55 60	
GAT GAA GAA AAC ACC GGA GCG GAC AGG CTG ATG ACT CAG AGG TGT AAG	240
Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys	
65 70 75 80	
GAC AAG TTG AAC GCT TTG GCC ATC TCG GTG ATG AAC CAG TGG CCA GGA	288
Asp Lys Leu Asn Ala Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly	
85 90 95	
GTG AAA CTG CGG GTG ACC GAG GGC TGG GAC GAA GAT GGC CAC CAC TCA	336
Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser	
100 105 110	
GAG GAG TCT CTG CAC TAC GAG GGC CGC GCA GTG GAC ATC ACC ACG TCT	384
Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser	
115 120 125	
GAC CGC GAC CGC AGC AAG TAC GGC ATG CTG GCC CGC CTG GCG GTG GAG	432
Asp Arg Asp Arg Ser Lys Tyr Gly Met Leu Ala Arg Leu Ala Val Glu	
130 135 140	
GCC GGC TTC GAC TGG GTG TAC TAC GAG TCC AAG GCA CAT ATC CAC TGC	480
Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys	
145 150 155 160	
TCG GTG AAA GCA GAG AAC TCG GTG GCG GCC AAA TCG GGA GGC	522
Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly	
165 170 174	

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCCAGGGTGT GAGCAACAGT

20

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGTGCTGCTT GGCACCTCTTG

20

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) strandedness: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CCGTGGCATT TCCCGGAAAG

20

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) strandedness: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GTATCCATGG CTCTCCTG

18

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) strandedness: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GCCTCGAGGT ATCCATGGCT CTCCTG

26

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) strandedness: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GCGCGGCCGC TCAGCCGCCC GCCCGGAC

28

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) strandedness: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CGTGTCGGTC AAAGCTGATA

20

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATGCATTCCA GTCGGCTGGA

20

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AAGGATCCGT CGACAAGCTT AATACGACGA ATTCTGGAGT TTTTTTTTTT TTTTTT

56

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGCTTCGACT GGGTCTACTA

20

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AAGGATCCGT CGACAAG

17

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATGCGCTTCG GCCAGCG 17

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GACAAGCTTA ATACGAC 17

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GTTGCGCCCG CTCACCG 17

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TACGACGAAT TCTGGAGT 18

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CCCGGAATT CATTGCGGGC CGGGCCGGGG GCCG 34

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) strandedness: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ACGATGAATT CTCAGCCGCC CGCCCGGACC GCCA

34

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) strandedness: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Ser Pro Gly Ile His  
1 5

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) strandedness: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CCCGGGAATT CATTGCGGAC CGGGCAGGGG GTT

33

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) strandedness: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ACGATGAATT CTCAGCCTCC CGATTGGCC GC

32